

### **INPUT SET: S1679.raw**

**This Raw Listing contains the General Information Section and up to the first 5 pages.**

SEQUENCE LISTING

1  
2  
3 (1) General Information:  
4  
5 (i) APPLICANT: Kaushansky, Kenneth  
6  
7 (ii) TITLE OF INVENTION: Methods of Stimulating Ery  
8 Using Hematopoietic Proteins.  
9  
10 (iii) NUMBER OF SEQUENCES: 6  
11  
12 (iv) CORRESPONDENCE ADDRESS:  
13 (A) ADDRESSEE: ZymoGenetics, Inc.  
14 (B) STREET: 1201 Eastlake Avenue East  
15 (C) CITY: Seattle  
16 (D) STATE: WA  
17 (E) COUNTRY: USA  
18 (F) ZIP: 98102  
19  
20 (v) COMPUTER READABLE FORM:  
21 (A) MEDIUM TYPE: Floppy disk  
22 (B) COMPUTER: IBM PC compatible  
23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
24 (D) SOFTWARE: PatentIn Release #1.0, Version  
25  
26 (vi) CURRENT APPLICATION DATA:  
27 (A) APPLICATION NUMBER:  
28 (B) FILING DATE:  
29 (C) CLASSIFICATION:  
30  
31 (viii) ATTORNEY/AGENT INFORMATION:  
32 (A) NAME: Parker, Gary E  
33 (B) REGISTRATION NUMBER: 31-648  
34 (C) REFERENCE/DOCKET NUMBER: 94-09C2  
35  
36 (ix) TELECOMMUNICATION INFORMATION:  
37 (A) TELEPHONE: 206-442-6673  
38 (B) TELEFAX: 206-442-6678  
39  
40  
41 (2) INFORMATION FOR SEQ ID NO:1:  
42  
43 (i) SEQUENCE CHARACTERISTICS:  
44 (A) LENGTH: 1062 base pairs  
45 (B) TYPE: nucleic acid  
46 (C) STRANDEDNESS: double

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47 (D) TOPOLOGY: linear

48

49 (ii) MOLECULE TYPE: cDNA

50

51

52 (ix) FEATURE:

53

(A) NAME/KEY: CDS

54

(B) LOCATION: 1..1059

55

56

57 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

58

59	ATG GAG CTG ACT GAA TTG CTC CTC GTG GTC ATG CTT CTC CTA ACT GCA	48
60	Met Glu Leu Thr Glu Leu Leu Val Val Met Leu Leu Leu Thr Ala	
61	1 5 10 15	
62	63 AGG CTA ACG CTG TCC AGC CCG GCT CCT CCT GCT TGT GAC CTC CGA GTC	96
64	Arg Leu Thr Leu Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val	
65	20 25 30	
66	67 CTC AGT AAA CTG CTT CGT GAC TCC CAT GTC CTT CAC AGC AGA CTG AGC	144
68	Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser	
69	35 40 45	
70	71 CAG TGC CCA GAG GTT CAC CCT TTG CCT ACA CCT GTC CTG CTG CCT GCT	192
72	Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala	
73	50 55 60	
74	75 GTG GAC TTT AGC TTG GGA GAA TGG AAA ACC CAG ATG GAG GAG ACC AAG	240
76	Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys	
77	65 70 75 80	
78	79 GCA CAG GAC ATT CTG GGA GCA GTG ACC CTT CTG CTG GAG GGA GTG ATG	288
80	Ala Gln Asp Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met	
81	85 90 95	
82	83 GCA GCA CGG GGA CAA CTG GGA CCC ACT TGC CTC TCA TCC CTC CTG GGG	336
84	Ala Ala Arg Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly	
85	100 105 110	
86	87 CAG CTT TCT GGA CAG GTC CGT CTC CTC CTT GGG GCC CTG CAG AGC CTC	384
88	Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu	
89	115 120 125	
90	91 CTT GGA ACC CAG CTT CCT CCA CAG GGC AGG ACC ACA GCT CAC AAG GAT	432
92	Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp	
93	130 135 140	
94	95 CCC AAT GCC ATC TTC CTG AGC TTC CAA CAC CTG CTC CGA GGA AAG GTG	480
96	Pro Asn Ala Ile Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val	
97	145 150 155 160	
98	99 CGT TTC CTG ATG CTT GTA GGA GGG TCC ACC CTC TGC GTC AGG CGG GCC	528

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100	Arg Phe Leu Met Leu Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala	
101	165	170
102		175
103	CCA CCC ACC ACA GCT GTC CCC AGC AGA ACC TCT CTA GTC CTC ACA CTG	576
104	Pro Pro Thr Thr Ala Val Pro Ser Arg Thr Ser Leu Val Leu Thr Leu	
105	180	185
106	190	
107	AAC GAG CTC CCA AAC AGG ACT TCT GGA TTG TTG GAG ACA AAC TTC ACT	624
108	Asn Glu Leu Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr Asn Phe Thr	
109	195	200
110	205	
111	AAC GAG CTC CCA AAC AGG ACT TCT GGA TTG TTG GAG ACA AAC TTC ACT	672
112	Asn Glu Leu Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr Asn Phe Thr	
113	210	215
114	220	
115	GCC TCA GCC AGA ACT ACT GGC TCT GGG CTT CTG AAG TGG CAG CAG GGA	720
116	Ala Ser Ala Arg Thr Thr Gly Ser Gly Leu Leu Lys Trp Gln Gln Gly	
117	225	230
118	235	240
119	TTC AGA GCC AAG ATT CCT GGT CTG CTG AAC CAA ACC TCC AGG TCC CTG	768
120	Phe Arg Ala Lys Ile Pro Gly Leu Leu Asn Gln Thr Ser Arg Ser Leu	
121	245	250
122	255	
123	GAC CAA ATC CCC GGA TAC CTG AAC AGG ATA CAC GAA CTC TTG AAT GGA	816
124	Asp Gln Ile Pro Gly Tyr Leu Asn Arg Ile His Glu Leu Leu Asn Gly	
125	260	265
126	270	
127	ACT CGT GGA CTC TTT CCT GGA CCC TCA CGC AGG ACC CTA GGA GCC CCG	864
128	Thr Arg Gly Leu Phe Pro Gly Pro Ser Arg Arg Thr Leu Gly Ala Pro	
129	275	280
130	285	
131	GAC ATT TCC TCA GGA ACA TCA GAC ACA GGC TCC CTG CCA CCC AAC CTC	912
132	Asp Ile Ser Ser Gly Thr Ser Asp Thr Gly Ser Leu Pro Pro Asn Leu	
133	290	295
134	300	
135	CAG CCT GGA TAT TCT CCT TCC CCA ACC CAT CCT CCT ACT GGA CAG TAT	960
136	Gln Pro Gly Tyr Ser Pro Ser Pro Thr His Pro Pro Thr Gly Gln Tyr	
137	305	310
138	315	320
139	ACG CTC TTC CCT CTT CCA CCC ACC TTG CCC ACC CCT GTG GTC CAG CTC	1008
140	Thr Leu Phe Pro Leu Pro Pro Thr Leu Pro Thr Pro Val Val Gln Leu	
141	325	330
142	335	
143	CAC CCC CTG CTT CCT GAC CCT TCT GCT CCA ACG CCC ACC CCT ACC AGC	1056
144	His Pro Leu Leu Pro Asp Pro Ser Ala Pro Thr Pro Thr Pro Thr Ser	
145	340	345
146	350	
147	GGG TAA	1062
148	Gly	
149		
150		
151		
152	(2) INFORMATION FOR SEQ ID NO:2:	

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153  
154 (i) SEQUENCE CHARACTERISTICS:  
155 (A) LENGTH: 353 amino acids  
156 (B) TYPE: amino acid  
157 (D) TOPOLOGY: linear  
158  
159 (ii) MOLECULE TYPE: protein  
160  
161 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:  
162  
163 Met Glu Leu Thr Glu Leu Leu Leu Val Val Met Leu Leu Leu Thr Ala  
164 1 5 10 15  
165  
166 Arg Leu Thr Leu Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val  
167 20 25 30  
168  
169 Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser  
170 35 40 45  
171  
172 Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala  
173 50 55 60  
174  
175 Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys  
176 65 70 75 80  
177  
178 Ala Gln Asp Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met  
179 85 90 95  
180  
181 Ala Ala Arg Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly  
182 100 105 110  
183  
184 Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu  
185 115 120 125  
186  
187 Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp  
188 130 135 140  
189  
190 Pro Asn Ala Ile Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val  
191 145 150 155 160  
192  
193 Arg Phe Leu Met Leu Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala  
194 165 170 175  
195  
196 Pro Pro Thr Thr Ala Val Pro Ser Arg Thr Ser Leu Val Leu Thr Leu  
197 180 185 190  
198  
199 Asn Glu Leu Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr Asn Phe Thr  
200 195 200 205  
201  
202 Ala Ser Ala Arg Thr Thr Gly Ser Gly Leu Leu Lys Trp Gln Gln Gly  
203 210 215 220  
204  
205 Phe Arg Ala Lys Ile Pro Gly Leu Leu Asn Gln Thr Ser Arg Ser Leu

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206 225 230 235 240  
207  
208 Asp Gln Ile Pro Gly Tyr Leu Asn Arg Ile His Glu Leu Leu Asn Gly  
209 245 250 255  
210  
211 Thr Arg Gly Leu Phe Pro Gly Pro Ser Arg Arg Thr Leu Gly Ala Pro  
212 260 265 270  
213  
214 Asp Ile Ser Ser Gly Thr Ser Asp Thr Gly Ser Leu Pro Pro Asn Leu  
215 275 280 285  
216  
217 Gln Pro Gly Tyr Ser Pro Ser Pro Thr His Pro Pro Thr Gly Gln Tyr  
218 290 295 300  
219  
220 Thr Leu Phe Pro Leu Pro Pro Thr Leu Pro Thr Pro Val Val Gln Leu  
221 305 310 315 320  
222  
223 His Pro Leu Leu Pro Asp Pro Ser Ala Pro Thr Pro Thr Pro Thr Ser  
224 325 330 335  
225  
226 Pro Leu Leu Asn Thr Ser Tyr Thr His Ser Gln Asn Leu Ser Gln Glu  
227 340 345 350  
228  
229 Gly  
230  
231  
232 (2) INFORMATION FOR SEQ ID NO:3:  
233  
234 (i) SEQUENCE CHARACTERISTICS:  
235 (A) LENGTH: 1486 base pairs  
236 (B) TYPE: nucleic acid  
237 (C) STRANDEDNESS: double  
238 (D) TOPOLOGY: linear  
239  
240 (ii) MOLECULE TYPE: cDNA  
241  
242 (vii) IMMEDIATE SOURCE:  
243 (B) CLONE: 1081  
244  
245 (ix) FEATURE:  
246 (A) NAME/KEY: CDS  
247 (B) LOCATION: 105..1241  
248  
249  
250 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:  
251  
252  
253 CCTCGTGCCG GTCCTGAGGC CCTTCTCCAC CCGGACAGAG TCCTTGGCCC ACCTCTCTCC 60  
254  
255 CACCGGACTC TGCCGAAAGA AGCACAGAAG CTCAAGCCGC CTCC ATG GCC CCA GGA 116  
256 Met Ala Pro Gly  
257  
258 1

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**SEQUENCE VERIFICATION REPORT**  
PATENT APPLICATION **US/08/347,748**

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Line

Error

Original Text